STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/926,493
Source: IFW P
Date Processed by STIC: 3/14/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/926,493

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2✓____Invalid Line Length
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213> Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11✓____Use of <220>
Sequence(s) 1-4 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa
"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

IFWP

RAW SEQUENCE LISTING DATE: 03/14/2006
PATENT APPLICATION: **US/09/926,493** TIME: 10:53:43

see item 2 on Error Summary Sheet

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03142006\I926493.raw**

3 <110> APPLICANT: Centre National De La Recherche Scientifique (CNRS)
5 <120> TITLE OF INVENTION: Nucleic Acid-Antibody Conjugate for Delivering A Foreign Nucleic Acid
6 into Cells
8 <130> FILE REFERENCE: P67289US0
10 <140> CURRENT APPLICATION NUMBER: US 09/926,493
C--> 12 <141> CURRENT FILING DATE: 2001-11-13
14 <150> PRIOR APPLICATION NUMBER: FR 99/05943
16 <151> PRIOR FILING DATE: 1999-05-10
E--> 18 <160> NUMBER OF SEQ ID NOS: 2 5 (p.4)
20 <170> SOFTWARE: PatentIn version 3.1

pp 1, 3-4

ERRORED SEQUENCES

9 shown below

Does Not Comply
Corrected Diskette Needed

22 <210> SEQ ID NO: 1
24 <211> LENGTH: 8
26 <212> TYPE: PRT
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
32 <221> NAME/KEY: MISC_FEATURE
34 <222> LOCATION: (1)...(2)
36 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of the antibody
38 <400> SEQUENCE: 1
W--> 40 Xaa Xaa Phe Tyr Gly Gly Phe Arg Leu
E--> 41 1 5

needs explanation in <2207-<2237 section / see item 11 on Error Summary Sheet)

see item 2 on Error Summary Sheet

44 <210> SEQ ID NO: 2
46 <211> LENGTH: 8
48 <212> TYPE: PRT
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
54 <221> NAME/KEY: MISC_FEATURE
56 <222> LOCATION: (1)...(2)
58 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of the antibody
60 <400> SEQUENCE: 2
W--> 62 Xaa Xaa Leu Tyr Gly Gly Phe Arg Leu
E--> 63 1 5

9 shown

needs explanation

see item 2 on Error Summary Sheet

66 <210> SEQ ID NO: 3
68 <211> LENGTH: 8
70 <212> TYPE: PRT
72 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:

9 (p.3)

needs explanation

76 <221> NAME/KEY: MISC_FEATURE
78 <222> LOCATION: (1)...(2)

RAW SEQUENCE LISTING DATE: 03/14/2006
PATENT APPLICATION: **US/09/926,493** TIME: 10:53:43

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03142006\I926493.raw**

80 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of the antibody
82 <400> SEQUENCE: 3
W--> 84 Xaa Xaa Tyr Leu Gly Gly Phe Arg Leu
E--> 85 1 5
88 <210> SEQ ID NO: 4
90 <211> LENGTH: 8 9
92 <212> TYPE: PRT
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
98 <221> NAME/KEY: MISC_FEATURE
100 <222> LOCATION: (1)...(2)
102 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of the antibody
104 <400> SEQUENCE: 4
W--> 106 Xaa Xaa Phe Phe Gly Gly Phe Arg Leu
E--> 107 1 5

see item 2 on Error Summary Sheet

needs explanation

see item 2 on Error Summary Sheet

<210> 5 last sequence in submitted file

<211> 39

<212> PRT

<213> Haemophilus influenzae

<220>

<223> Biotinylated hemagglutinin fusogenic peptide

<400> 5

```
Gly Leu Phe Glu Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly
1               5                  10                  15
Met Ile Asp Gly Gly Gly Cys Gly Ser Gly Ser Tyr Thr Asp Ile Glu
            20                  25                  30
Met Asn Arg Leu Gly Lys Gly
        35
```

5

VERIFICATION SUMMARY DATE: 03/14/2006
PATENT APPLICATION: **US/09/926,493** TIME: 10:53:44

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03142006\I926493.raw**

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:41 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:1
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:63 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:2
L:84 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:85 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:107 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:4
L:18 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (2) Counted (5)